



#5

SEQUENCE LISTING

<110> Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING THYROID
STIMULATING HORMONE RECEPTOR (TSH-R) GENE DISRUPTIONS

<130> R-666

<150> US 60/243,895

<151> 2000-10-26

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2512

<212> DNA

<213> Mus musculus

<400> 1

```

cagcagcaga cgcagggcac tgagaatgag cgacagcgcg caacgatgaa gtagcccaga 60
gggtcccttg gaaaatgagg caggggcccc tgcctgctgt tgttctgctg ctgcacctgt 120
ccaggagcct ggcgggcaaa gagtgtgcgt ctccacctgt tgagtgtcac caggaggacg 180
acttcagagt cactggaag gagctccacc gaatccccag cctgccgccc agcaccaga 240
ctctgaagct catcgagact catctgaaga ccatacccag tcttgcatth tcgagtctgc 300
ccaacttttc caggatctat ttatctatag atgcaactct gcagcggctg gaaccacatt 360
ctttctacaa tttgagtaaa atgactcaca tagaaatccg gaacaccaga agcttaacct 420
atatagacce tgatgccttg acagagctcc ccttgctcaa gtttcttgge attttcaata 480
ctggacttag aatattccct gacttgacca aaattttatt cacggacata ttctttatac 540
ttgaaatcac agacaacct tacatgactt cggctccctga aaacgcattc cagggcctat 600
gcaatgaaac cttgaccctg aaactgtaca acaatggatt tacttcagtc caaggacatg 660
ctttcaatgg aacaaagctg gatgctgttt acctaaacaa gaataaatac ctgacagcta 720
tagacaacga tgcctttgga ggagtataca gtggaccaac tttgctagat gtgtcttcca 780
ccagcgtcac tgccttccct tccaaaggcc tggagcacct caaagaactg atcgcaaaag 840
acacctggac tctcaaaaag ctcccgtgtt cgttgagttt cctccacctc actcgggctg 900
acctctctta cccgagccac tgctgcgctt ttaagaacca gaagaaaatc aggggaatcc 960
tggagtcttt gatgtgtaat gagagcagta tccggaacct tcgtcaaagg aaatcagtga 1020
acatcttgag ggtcccatc taccaggaat atgaagaaga tccgggtgac aacagtgttg 1080
ggtacaaaca aaactccaag ttccaggaga gcccaagcaa ctctcactat tacgtcttct 1140
ttgaagaaca agaggatgag gtcgttggtt tccggccaaga gctcaaaaat cctcaggaag 1200
agactctcca agccttcgag agccactatg actacacggt gtgtggggac aacgaggaca 1260
tggtgtgtac cccaagtcg gacgagttha acccctgtga agatatcatg ggctacaggt 1320
tcttgagaat cgtggtgtgg tttgtcagtc tgctggctct cctgggcaat atcttcgtcc 1380
tgctcattct gctaaccagc cactacaaat tgaccgtgcc gcggttctc atgtgcaact 1440
tggcctttgc agatttctgc atgggggtat acctgcttct cattgcctct gtagacctgt 1500
acacacactc tgagtactac aaccacgcca tcgactggca gacgggccct ggggtgcaaca 1560
cggctggctt cttcactgtt ttccgccagt agttatcagt gtacacactg acggtcatca 1620
ccctggagcg atggtacgcc atcaccttcg ccattgcgct ggataggaag atccgcctca 1680
ggcacgcgta caccatcatg gctggggggt ggggttccct ctctctctc gccctgctcc 1740
cgatggtggg aatcagcagc tatgccaagg tcagcatctg cctgccaatg gacaccgaca 1800
cccctcttgc actcgcatac attgtcctcg ttctgctgct caatgttggt gcctttgttg 1860
tcgtctgttc ctgctatgtg aagatctaca tcacgggtccg aaatccccag tacaacctc 1920
gagataaaga caccaagatt gccaaagagga tggctgtgtt gatcttcaat gacttcatgt 1980
gcatggcgcc catctccttc tatgcgctgt cggcacttat gaacaagcct ctaatcactg 2040
ttactaactc caaaatcttg ttggttctct tctacccctt caactcctgt gccaatccgt 2100
ttctctatgc tattttcacc aaggccttcc agagggacgt gttcactctg ctcagcaagt 2160
ttggcatctg caaacgccag gcccaggcct atcagggtca gagagtctgt cccaacaata 2220

```

gcactggtat tcagatccaa aagattcccc aggacacgag gcagagtctc cccaacatgc 2280
aagataccta tgaactgctt ggaaactccc agctagctcc aaaactgcag ggacaaatct 2340
cagaagagta taagcaaaca gccttgtaaa ggaaaggcta cgctagtcac agtgagactt 2400
acaaaaggct ggtttcttga acatgcgttc cagtcctcgtg acatgtgaac acatagggttc 2460
atgcaggtga tgattcatag ggtcagagtt catctctaga aagtattgcc tc 2512

<210> 2

<211> 764

<212> PRT

<213> Mus musculus

<400> 2

Met	Arg	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Val	Leu	Leu	Leu	Ala	Leu	Ser
1				5					10					15	
Arg	Ser	Leu	Arg	Gly	Lys	Glu	Cys	Ala	Ser	Pro	Pro	Cys	Glu	Cys	His
			20					25					30		
Gln	Glu	Asp	Asp	Phe	Arg	Val	Thr	Cys	Lys	Glu	Leu	His	Arg	Ile	Pro
		35					40					45			
Ser	Leu	Pro	Pro	Ser	Thr	Gln	Thr	Leu	Lys	Leu	Ile	Glu	Thr	His	Leu
	50					55					60				
Lys	Thr	Ile	Pro	Ser	Leu	Ala	Phe	Ser	Ser	Leu	Pro	Asn	Ile	Ser	Arg
65					70					75					80
Ile	Tyr	Leu	Ser	Ile	Asp	Ala	Thr	Leu	Gln	Arg	Leu	Glu	Pro	His	Ser
			85						90					95	
Phe	Tyr	Asn	Leu	Ser	Lys	Met	Thr	His	Ile	Glu	Ile	Arg	Asn	Thr	Arg
			100					105						110	
Ser	Leu	Thr	Tyr	Ile	Asp	Pro	Asp	Ala	Leu	Thr	Glu	Leu	Pro	Leu	Leu
		115					120					125			
Lys	Phe	Leu	Gly	Ile	Phe	Asn	Thr	Gly	Leu	Arg	Ile	Phe	Pro	Asp	Leu
	130					135					140				
Thr	Lys	Ile	Tyr	Ser	Thr	Asp	Ile	Phe	Phe	Ile	Leu	Glu	Ile	Thr	Asp
145					150					155					160
Asn	Pro	Tyr	Met	Thr	Ser	Val	Pro	Glu	Asn	Ala	Phe	Gln	Gly	Leu	Cys
			165						170					175	
Asn	Glu	Thr	Leu	Thr	Leu	Lys	Leu	Tyr	Asn	Asn	Gly	Phe	Thr	Ser	Val
			180					185					190		
Gln	Gly	His	Ala	Phe	Asn	Gly	Thr	Lys	Leu	Asp	Ala	Val	Tyr	Leu	Asn
		195					200					205			
Lys	Asn	Lys	Tyr	Leu	Thr	Ala	Ile	Asp	Asn	Asp	Ala	Phe	Gly	Gly	Val
	210					215					220				
Tyr	Ser	Gly	Pro	Thr	Leu	Leu	Asp	Val	Ser	Ser	Thr	Ser	Val	Thr	Ala
225					230					235					240
Leu	Pro	Ser	Lys	Gly	Leu	Glu	His	Leu	Lys	Glu	Leu	Ile	Ala	Lys	Asp
			245						250					255	
Thr	Trp	Thr	Leu	Lys	Lys	Leu	Pro	Leu	Ser	Leu	Ser	Phe	Leu	His	Leu
			260					265					270		
Thr	Arg	Ala	Asp	Leu	Ser	Tyr	Pro	Ser	His	Cys	Cys	Ala	Phe	Lys	Asn
		275					280					285			
Gln	Lys	Lys	Ile	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Met	Cys	Asn	Glu	Ser
	290					295					300				
Ser	Ile	Arg	Asn	Leu	Arg	Gln	Arg	Lys	Ser	Val	Asn	Ile	Leu	Arg	Gly
305					310					315					320
Pro	Ile	Tyr	Gln	Glu	Tyr	Glu	Glu	Asp	Pro	Gly	Asp	Asn	Ser	Val	Gly
			325						330					335	
Tyr	Lys	Gln	Asn	Ser	Lys	Phe	Gln	Glu	Ser	Pro	Ser	Asn	Ser	His	Tyr
			340					345					350		
Tyr	Val	Phe	Phe	Glu	Glu	Gln	Glu	Asp	Glu	Val	Val	Gly	Phe	Gly	Gln
		355					360					365			
Glu	Leu	Lys	Asn	Pro	Gln	Glu	Glu	Thr	Leu	Gln	Ala	Phe	Glu	Ser	His
	370					375					380				
Tyr	Asp	Tyr	Thr	Val	Cys	Gly	Asp	Asn	Glu	Asp	Met	Val	Cys	Thr	Pro

385		390		395		400									
Lys	Ser	Asp	Glu	Phe	Asn	Pro	Cys	Glu	Asp	Ile	Met	Gly	Tyr	Arg	Phe
		405							410					415	
Leu	Arg	Ile	Val	Val	Trp	Phe	Val	Ser	Leu	Leu	Ala	Leu	Leu	Gly	Asn
		420							425					430	
Ile	Phe	Val	Leu	Leu	Ile	Leu	Leu	Thr	Ser	His	Tyr	Lys	Leu	Thr	Val
		435							440					445	
Pro	Arg	Phe	Leu	Met	Cys	Asn	Leu	Ala	Phe	Ala	Asp	Phe	Cys	Met	Gly
		450							455					460	
Val	Tyr	Leu	Leu	Leu	Ile	Ala	Ser	Val	Asp	Leu	Tyr	Thr	His	Ser	Glu
465					470					475					480
Tyr	Tyr	Asn	His	Ala	Ile	Asp	Trp	Gln	Thr	Gly	Pro	Gly	Cys	Asn	Thr
			485						490					495	
Ala	Gly	Phe	Phe	Thr	Val	Phe	Ala	Ser	Glu	Leu	Ser	Val	Tyr	Thr	Leu
		500							505					510	
Thr	Val	Ile	Thr	Leu	Glu	Arg	Trp	Tyr	Ala	Ile	Thr	Phe	Ala	Met	Arg
		515							520					525	
Leu	Asp	Arg	Lys	Ile	Arg	Leu	Arg	His	Ala	Tyr	Thr	Ile	Met	Ala	Gly
		530							535					540	
Gly	Trp	Val	Ser	Cys	Phe	Leu	Leu	Ala	Leu	Leu	Pro	Met	Val	Gly	Ile
545					550					555					560
Ser	Ser	Tyr	Ala	Lys	Val	Ser	Ile	Cys	Leu	Pro	Met	Asp	Thr	Asp	Thr
			565						570					575	
Pro	Leu	Ala	Leu	Ala	Tyr	Ile	Val	Leu	Val	Leu	Leu	Leu	Asn	Val	Val
		580							585					590	
Ala	Phe	Val	Val	Val	Cys	Ser	Cys	Tyr	Val	Lys	Ile	Tyr	Ile	Thr	Val
		595							600					605	
Arg	Asn	Pro	Gln	Tyr	Asn	Pro	Arg	Asp	Lys	Asp	Thr	Lys	Ile	Ala	Lys
		610							615					620	
Arg	Met	Ala	Val	Leu	Ile	Phe	Thr	Asp	Phe	Met	Cys	Met	Ala	Pro	Ile
625					630					635					640
Ser	Phe	Tyr	Ala	Leu	Ser	Ala	Leu	Met	Asn	Lys	Pro	Leu	Ile	Thr	Val
			645						650					655	
Thr	Asn	Ser	Lys	Ile	Leu	Leu	Val	Leu	Phe	Tyr	Pro	Leu	Asn	Ser	Cys
			660						665					670	
Ala	Asn	Pro	Phe	Leu	Tyr	Ala	Ile	Phe	Thr	Lys	Ala	Phe	Gln	Arg	Asp
		675							680					685	
Val	Phe	Ile	Leu	Leu	Ser	Lys	Phe	Gly	Ile	Cys	Lys	Arg	Gln	Ala	Gln
		690							695					700	
Ala	Tyr	Gln	Gly	Gln	Arg	Val	Cys	Pro	Asn	Asn	Ser	Thr	Gly	Ile	Gln
705					710					715					720
Ile	Gln	Lys	Ile	Pro	Gln	Asp	Thr	Arg	Gln	Ser	Leu	Pro	Asn	Met	Gln
			725						730					735	
Asp	Thr	Tyr	Glu	Leu	Leu	Gly	Asn	Ser	Gln	Leu	Ala	Pro	Lys	Leu	Gln
			740						745					750	
Gly	Gln	Ile	Ser	Glu	Glu	Tyr	Lys	Gln	Thr	Ala	Leu				
		755							760						

<210> 3

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting vector

<400> 3

acttgagagc ctctccttcc ccctctccag cgtgctctcc agcgatgagg tcacagcccc 60
tcggagccct cctcctccct cccttcccct cctgcacccg ggtctcttcc agcgtcagac 120
gcagggcact gagaatgtgg cgacagcgcg caacgatgaa gtagcccaga gggtccttg 180

gaaaatgagg ccagggtccc

200

<210> 4

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting vector

<400> 4

gtgtcaccag	gaggacgact	tcagagtcac	ctgcaaggag	ctccaccgaa	tccccagcct	60
gccgcccagc	accagactc	tgtgagtagc	caaggccaag	accccccccc	cccgagaaat	120
tcgtggtgtg	tggtgggggtg	tgcgcggata	tctggtcagt	ccctgtacaa	attcaatccc	180
ccatgctcgg	gaaggtcagc					200